

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.
 Baker, Kevin
 Chuntharapai, Anan
 Gurney, Austin
 Kim, Kyung Jin
10 Wood, William

(ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

15 (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
20 (D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

25 (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

30 (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
(B) FILING DATE: 12-Jun-1998
(C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

5 (A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110P1

10 (ix) TELECOMMUNICATION INFORMATION:

10 (A) TELEPHONE: 650/225-5416

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

15 (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
1 5 10 15

Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
20 25 30

Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Arg
35 40 45

30 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
50 55 60

Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65 70 75

Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
80 85 90

Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
5 95 100 105

Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
110 115 120

10 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
125 130 135

Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
140 145 150

15 Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
155 160 165

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
20 170 175 180

Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
185 190 195

25 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
200 205 210

Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
215 220 225

30 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
230 235 240

Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
35 245 250 255

Ile Val Phe Val

259

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- 10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15 GCTGTGGAA CCTCTCCACG CGCACGAAC CAGCCAACGA TTTCTGATAG 50

ATTTTGAAA GTTGACCAAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100

CGTTAGGGAA CTCTGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150

20 AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCAT A C ATG 195
Met

1

25 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234
Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile

5 10

30 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273
Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

15 20 25

35 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312
Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

30 35 40

CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351
Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
45 50

5 CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390
Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
55 60 65

10 AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429
Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
70 75

15 AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468
Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
80 85 90

20 TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA 507
Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
95 100 105

25 GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT 546
Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
110 115

30 GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC 585
Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
120 125 130

35 CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG 624
Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
135 140

GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC 663
Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
35 145 150 155

ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702
Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
160 165 170

5 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
175 180

10 AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780
Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
185 190 195

15 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
200 205

20 GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858
Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
210 215 220

25 GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897
Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
225 230 235

30 GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936
Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
240 245

ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCCTTC CTTACCTGAA AGGTTCAAGGT 1020

35 AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCCTCCC 1070

TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCC CAAAAAAA 1120

AAAAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1170

5 AAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly

-40 -35 -30

20 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro

-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro

-10 -5 1 5

25 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro

10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro

25 30 35

30 Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly

40 45 50

35 Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala

55 60 65

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
70 75 80

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
5 85 90 95

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
100 105 110

10 Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
115 120 125

Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
130 135 140

15 Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
145 150 155

Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
20 160 165 170

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
175 180 185

25 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
190 195 200

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
205 210 215

30 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
220 225 230

Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
35 235 240 245

Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- 10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTTGACCAG AG ATG CAA GGG GTG AAG GAG 90
Met Gln Gly Val Lys Glu
-40 -35

20 CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
-30 -25

25 CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168
Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
-20 -15 -10

30 CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-5 1 5

AAG ACC CTA AAG TTC GTC GTC ATC GTC GCG GTC CTG 246
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
35 10 15

CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG 285
Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
20 25 30

5 GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG 324
Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
35 40

10 AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT 363
Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
45 50 55

15 CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA 402
His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
60 65 70

20 GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT 441
Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
75 80

25 TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA 480
Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
85 90 95

30 CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT 519
His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
100 105

35 CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA 558
Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
110 115 120

40 GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA 597
Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
125 130 135

GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
140 145

5 TGT GTT GAA GAA TTT GGT GCC AAT GCC ACT GTG GAA ACC 675
Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
150 155 160

CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCG GGG ACT 714
10 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
165 170

CCT GCC CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCA 753
Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro
150 175 180 185

GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC 792
Gly Thr Pro Ala Pro Ala Glu Glu Thr Met Thr Thr
190 195 200

20 AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 831
Ser Pro Gly Thr Pro Ala Pro Ala Glu Glu Thr Met
205 210

25 ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG 870
Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Glu Glu
215 220 225

ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC TCT TCT CAT 909
30 Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
230 235

TAC CTC TCA TGC ACC ATC GTA GGG ATC ATA GTT CTA ATT 948
Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile
35 240 245 250

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990
Val Leu Leu Ile Val Phe Val
255 259

5 AAATTCCTTC CTTACCTGAA AGGTTCAGGT AGGCCTGGC TGAGGGCGGG 1040

GGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCACAGAC 1090

AGAACGCCT GCCCCTGCC CAAAAAAA AAAAAAAA AAAAAAAA 1140

10 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

25 (2) INFORMATION FOR SEQ ID NO:6:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His
1 5 10 15

15 Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly
20 25 30

Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys
35 40 45

Gly Cys Arg Lys
49

(2) INFORMATION FOR SEQ ID NO:8:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
5 35 40 45

Cys Lys Glu
48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
Met Glu
1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
10 Gln Arg Gly Gin Asn Ala Pro Ala Ala Ser Gly Ala Arg
5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
15 20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
30 35 40

20 GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
45 50

25 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
55 60 65

30 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
70 75 80

35 TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
85 90

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
95 100 105

5 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
110 115

10 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
120 125 130

15 AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
135 140 145

20 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
150 155

25 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
160 165 170

CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
175 180

30 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
185 190 195

35 GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
215 220

5 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
225 230 235

10 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
240 245

15 TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
250 255 260

20 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
265 270 275

25 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
290 295 300

30 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
305 310

35 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
315 320 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
345 350

TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
10 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
355 360 365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
15 370 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
380 385 390

20 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
25 Ala Asp Ser Ala Xaa Ser
410 411

CCTTCCCTGG TTTACCTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
30 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTCACTGCAC 1550

35 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTCAC AGCACTTTT TATCCTAATG TAAATGCTTT ATTTATTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAG AAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg

1 5 10 15

20

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro

20 25 30

25

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val

35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp

50 55 60

30

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser

65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp

80 85 90

35

Protein sequence

	Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr			
	95	100	105	
	His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp			
5		110	115	120
	Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr			
		125	130	135
10	Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro			
		140	145	150
	Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val			
		155	160	165
15	Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His			
		170	175	180
20	Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val			
		185	190	195
25	Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys			
		200	205	210
30	Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Asp			
		215	220	225
35	Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp			
		230	235	240
	Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val			
		245	250	255
	Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly			
		260	265	270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
5 290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

10 Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

15 Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

20 Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

25 Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

Ala Asp Ser Ala Xaa Ser
410 411

30

(2) INFORMATION FOR SEQ ID NO:12:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

15
20
25
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35
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45
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55
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65
70
75
80
85
90
95

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30